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          GENERAL INFORMATION SECTION

          3,<110> Thym, Detlef
          4,   Knappe, Wolfgang-Reinhold
          5,   Shao, Zhixin
          6,   Schmuck, Rainer
          7,   Kratzsch, Peter
          8,   Bunk, Daniella
          10,<120> New Forms of Soluble Pyrroloquinoline Quinone-
Dependent Glucose Dehydrogenase
          12,<130> RDID 00112CIPUS
          14,<150> EP 00123512.6
          15,<151> 2000-10-27
          17,<150> EP 00127294.7
          18,<151> 2000-12-19
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          21,<151> 2000-11-09
          23,<160> 26
          25,<170> PatentIn version 3.1

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          STATISTICS SUMMARY

     Application Serial Number:

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        Alpha or Numeric: Numeric
       Application Class:
   Application File Date:
               Art Unit:
    Software Application: PatentIn
Total Number of Sequences: 26
       Total Nucleotides: 6196
       Total Amino Acids: 930
        Number of Errors: 0
      Number of Warnings: 11
   Number of Corrections: 0
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<110> Thym, Detlef
       Knappe, Wolfgang-Reinhold
       Shao, Zhixin
       Schmuck, Rainer
       Kratzsch, Peter
       Bunk, Daniella

<120> New Forms of Soluble Pyrroloquinoline Quinone-Dependent Glucose Dehydrogenase

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aaaacagttt ttcaggtacc agagattgtc aatgatgctg atgggcagaa tggtttatta   240

ggttttgcct tccatcctga ttttaaaaat aatccttata tctatatttc aggtacattt   300

aaaaatccga atctacaga taaagaatta ccgaaccaaa cgattattcg tcgttatacc   360

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attggtgacc aagggcgtaa ccagcttgct tatttgttct tgccaaatca agcacaacat   540

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tttaagagca acaaccgtta tcgtgatgtg attgcaagtc cagatgggaa tgtcttatat   1260

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Lys Ile Leu Arg Val Asn Pro Glu Ser Gly Ser Val Lys Thr Val Phe
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Gln Val Pro Glu Ile Val Asn Asp Ala Asp Gly Gln Asn Gly Leu Leu
65                  70                  75                  80

Gly Phe Ala Phe His Pro Asp Phe Lys Asn Asn Pro Tyr Ile Tyr Ile
                85                  90                  95

Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
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Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Ser Thr Asp Thr Leu
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Glu Lys Pro Val Asp Leu Leu Ala Gly Leu Pro Ser Ser Lys Asp His
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Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
145                 150                 155                 160

Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
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Ser Ile Lys Asp Leu Ala Gln Asn Gly Val Lys Val Ala Ala Gly Val
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Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp Pro
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Asn Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg Ile
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Lys Leu Asp Pro Thr Tyr Ser Thr Thr Tyr Asp Asp Ala Val Pro Met
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Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Asp Gly
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Asn Val Leu Tyr Val Leu Thr Asp Thr Ala Gly Asn Val Gln Lys Asp
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            35   40   45

Lys Ile Leu Arg Val Asn Pro Val Ser Gly Ser Ala Lys Thr Val Phe
    50   55   60

Gln Val Pro Glu Ile Val Ser Asp Ala Asp Gly Gln Asn Gly Leu Leu
65   70   75   80

Gly Phe Ala Phe His Pro Asp Phe Lys His Asn Pro Tyr Ile Tyr Ile
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Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn
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Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Thr Thr Asp Thr Phe
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Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
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Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Ser Lys Asp Tyr
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His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Ile
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Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr
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Leu Leu Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu
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Val Leu Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys

                                     260   265   270

Asp Asp Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Thr Asn Lys
        275   280   285

Ser Gln Ile Lys Asp Leu Ala Gln Asn Gly Ile Lys Val Ala Thr Gly
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Pro Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp
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            340   345   350

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Ile Lys Leu Asp Pro Thr Tyr Ser Thr Thr Leu Asp Asp Ala Ile Pro
385   390   395   400

Met Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Glu
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